STIC Search Report
Biotech-Chem Library

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STIC
USPTO

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Wednesday, December 08, 2004

Case Serial Number: 09/903508

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

sira
Search and Information
Resources Administration

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            GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    December 7, 2004, 19:08:08 ; Search time 2509 Seconds
                    (without alignments)
                    9178.989 Million cell updates/sec

Title:          US-09-903-508A-3
Perfect score:  487
Sequence:       1 tgattacgaattcgagcctcg........agttcatgatttctgtta 487

Scoring table:  IDENTITY.NUC
                Gapop 10.0 , Gapext 1.0

Searched:       452729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters:    9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	457	93.8	1493	6	AX449214	AX449214 Sequence
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	4	211	43.3	7834	12	CVU33753	CVU33753 Yeast episo
	5	211	43.3	8001	6	AR344983	AR344983 Sequence
	6	211	43.3	10667	12	YEP213	U03499 Yeast episo
	7	211	43.3	11259	12	AF102576	AF102576 Cloning v
	8	206	42.3	937	8	YSCLEU2A	M12909 Yeast (S.ce
C	9	206	42.3	5558	12	CVPFL26	X70477 Integrative
C	10	206	42.3	6078	12	CVPFL46S	X70270 multicopy S
C	11	206	42.3	6369	12	CVPFL36	X70481 replicative
C	12	206	42.3	6461	12	XXU34315	U34315 E.coli/Kluy
C	13	206	42.3	7272	12	XXU34321	U34321 E.coli/Kluy
C	14	206	42.3	7561	12	XXU34313	U34313 E.coli/Kluy
C	15	206	42.3	7713	12	XXU34318	U34318 E.coli/Kluy
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	17	206	42.3	10667	12	YEP13	U03498 Yeast episo
C	18	206	42.3	11198	6	AR492048	AR492048 Sequence
C	19	206	42.3	11201	6	AR492050	AR492050 Sequence
C	20	206	42.3	11204	6	AR492051	AR492051 Sequence
C	21	206	42.3	11427	6	AR492049	AR492049 Sequence
C	22	206	42.3	12008	6	AR492052	AR492052 Sequence
C	23	206	42.3	12844	6	AR492044	AR492044 Sequence
C	24	206	42.3	12850	6	AR492047	AR492047 Sequence
C	25	206	42.3	12851	6	AR492046	AR492046 Sequence
C	26	206	42.3	13073	6	AR492045	AR492045 Sequence
C	27	206	42.3	13654	6	AR492053	AR492053 Sequence
C	28	206	42.3	316613	8	SCCHRIII	X59720 S.cerevisia
C	29	205	42.1	9414	12	AY297714	AY297714 Yeast tru
C	30	193.2	39.7	151780	12	AC150702	AC150702 Oryza sat
	31	193	39.6	53949	2	AC090724	AC090724 Homo sapi
	32	193	39.6	71120	2	AC124800	AC124800 Homo sapi
	33	193	39.6	110000	2	LMFLCHR15_3	Continuation (4 of
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	35	191.4	39.3	16011	12	XXU09128	U09128 pSacBII P1
	36	191.4	39.3	18772	12	AF133437	AF133437 Cloning v
	37	191.4	39.3	176781	2	AC002989	AC002989 Homo sapi
	38	189.8	39.0	6654	12	XXU35112	U35112 Synthetic E
	39	189.8	39.0	7596	12	AF347016	AF347016 Shuttle v
	40	189.8	39.0	8800	6	AX469663	AX469663 Sequence
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	42	189.8	39.0	9211	12	AF064066	AF064066 Expressio
	43	189.8	39.0	9215	12	AF049063	AF049063 Expressio
	44	189.8	39.0	9956	12	AF049064	AF049064 Expressio
	45	189.8	39.0	10042	6	AX469664	AX469664 Sequence

ALIGNMENTS

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LOCUS       AX449216                   487 bp    DNA    linear   PAT 03-JUL-2002
DEFINITION  Sequence 3 from Patent WO0206448.
ACCESSION   AX449216
VERSION     AX449216.1  GI:21697993
KEYWORDS
SOURCE      Debaryomyces hansenii (anamorph: Candida famata)
ORGANISM    Debaryomyces hansenii
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Debaryomyces.
REFERENCE   1
AUTHORS     Abbas,C.
TITLE       Transformation systems for flavinogenic yeast
JOURNAL     Patent: WO 0206448-A 3 24-JAN-2002;
            Abbas, Charles (US)
FEATURES    Location/Qualifiers
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ORIGIN

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Best Local Similarity   100.0%;  Pred. No. 3.3e-74;
Matches  487;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy         61 ATTTTTTTAACGATTTTTTAATAATTTTGCAATCATTTAAGAAAAACCACAAATGGTTTT 120
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Db         61 ATTTTTTTAACGATTTTTTAATAATTTTGCAATCATTTAAGAAAAACCACAAATGGTTTT 120

Qy        121 CCAAAATTAAATGATTTTTAGAAGTCCTAAAAATAGAATCATCAAAATAAGAA 180
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Qy        181 CAACTTAAAGTCACTATGACAAATTCAGAAATACAATCGTATGATCCGTTCATGGATAAA 240
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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title:           US-09-903-508A-3
Perfect score:   487
Sequence:        1 tgattacgaattcgagctcg.........agtttcatgattttctgtta 487

Scoring table:   IDENTITY.NUC
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Searched:        4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters:    8269772

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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5		206	42.3	11198	4	AAD07496	Aad07496 pYLR110P
6		206	42.3	11201	4	AAD07498	Aad07498 pYMR107P
7		206	42.3	11204	4	AAD07499	Aad07499 pZEO1P DN
8		206	42.3	11427	4	AAD07497	Aad07497 pYMR251AP
9		206	42.3	12008	4	AAD07500	Aad07500 pPR1BP DN
10		206	42.3	12844	4	AAD07492	Aad07492 pYLR110P+
11		206	42.3	12850	4	AAD07495	Aad07495 pZEO1P+lu
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13		206	42.3	13073	4	AAD07493	Aad07493 pYMR251AP
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18		177.8	36.5	7429	10	ADD02778	Add02778 Plasmid p
19		177.8	36.5	11713	3	AAC55501	Aac55501 Destinati
20		177.8	36.5	12288	3	AAC55629	Aac55629 Destinati
21	c	176.2	36.2	9952	10	ABV77349	Abv77349 Yeast exp
22		120	24.6	1494	8	AAD48348	Aad48348 Saccharom
23	c	84.8	17.4	10213	10	ADD02779	Add02779 Plasmid p
24	c	73.2	15.0	5161	4	AAF61508	Aaf61508 A. gossyp
25		71	14.6	1467	4	ABZ31929	Abz31929 Candida a
26	c	70.6	14.5	1473	10	ADF75062	Adf75062 A_gossypi
27	c	60.2	12.4	5615	11	ADM47088	Adm47088 Ogataea m
28		53	10.9	1554	8	ABT20720	Abt20720 Aspergill
29		53	10.9	1778	8	ABT20122	Abt20122 Aspergill
30		53	10.9	3140	8	ABT17712	Abt17712 Aspergill
31		53	10.9	3778	8	ABT19526	Abt19526 Aspergill
32	c	52.6	10.8	10250	6	ABN80083	Abn80083 Human che
33	c	51.4	10.6	76	12	ADM98299	Adm98299 PCR prime
34		51.2	10.6	2486	3	AAA97037	Aaa97037 Nucleotid
35	c	50.4	10.3	1373	2	AAV52969	Aav52969 Human G1
36	c	50.2	10.3	29993	10	ADB37662	Adb37662 Human che
37	c	50.2	10.3	29993	10	ADB37660	Adb37660 Human che
38	c	50.2	10.3	38342	4	AAS46745	Aas46745 Tumour su
39		50.2	10.3	38342	4	ABK31506	Abk31506 Signal tr
40		50	10.3	123	2	AAX87476	Aax87476 Plasmid p
41	c	50	10.3	6236	6	ABL33631	Abl33631 Human imm
42	c	50	10.3	6236	6	ABN80203	Abn80203 Human che
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44	c	47.8	9.8	61020	4	AAS46787	Aas46787 Tumour su
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ALIGNMENTS

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ID   AAL41986 standard; DNA; 487 BP.
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AC   AAL41986;
XX
DT   29-AUG-2003 (revised)
DT   13-MAY-2002 (first entry)
XX
DE   Candida famata VKM Y-9 ARS element (CfARS) 2.
XX
KW   VKM Y-9 ARS element; ds; autonomous replicating sequence element; CfARS;
KW   flavinogenic yeast transformation; electroporation;
KW   yeast cell spheroplast.
XX
OS   Debaryomyces hansenii.
XX
PN   WO20206448-A2.
XX
PD   24-JAN-2002.
XX
PF   13-JUL-2001; 2001WO-US022083.
XX
PR   14-JUL-2000; 2000US-0218244P.
PR   04-MAY-2001; 2001US-0288491P.
PR   15-MAY-2001; 2001US-0290667P.
XX
PA   (ABBA/) ABBAS C.
XX
PI   Abbas C;
XX
DR   WPI; 2002-148374/19.
XX
PT   A nucleic acid construct used in the transformation of the flavinogenic
PT   yeasts Pichia guilliermondii and Candida famata by electroporation and
PT   spheroplast formation.
XX
PS   Claim 2; Fig 20; 202pp; English.
XX
CC   The invention comprises the nucleotide sequences of three autonomous
CC   replicating sequence (ARS) elements. The invention also comprises methods
CC   for the transformation of yeast cells (e.g. flavinogenic yeast), one such
CC   method involves electroporating a yeast cell suspension, together with
CC   constructs containing the ARS elements of the invention. Another yeast
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OM nucleic - nucleic search, using sw model

Run on:        December  7, 2004, 20:18:39 ; Search time 78 Seconds
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                                            4437.874 Million cell updates/sec

Title:          US-09-903-508A-3
Perfect score:  487
Sequence:       1 tgattacgattcgagctcg.........agttcatgatttctgtta 487

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:        1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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              Pred. No. is the number of results predicted by chance to have a
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                                    SUMMARIES
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c 2	206	42.3	11198	4	US-09-743-194-23	Sequence 23, Appl
c 3	206	42.3	11201	4	US-09-743-194-25	Sequence 25, Appl
c 4	206	42.3	11204	4	US-09-743-194-26	Sequence 26, Appl
c 5	206	42.3	11427	4	US-09-743-194-24	Sequence 24, Appl
c 6	206	42.3	12008	4	US-09-743-194-27	Sequence 27, Appl
c 7	206	42.3	12844	4	US-09-743-194-19	Sequence 19, Appl
c 8	206	42.3	12850	4	US-09-743-194-22	Sequence 22, Appl
c 9	206	42.3	12851	4	US-09-743-194-21	Sequence 21, Appl
c 10	206	42.3	13073	4	US-09-743-194-20	Sequence 20, Appl
c 11	206	42.3	13654	4	US-09-743-194-28	Sequence 28, Appl
c 12	71	14.6	279	4	US-09-248-796A-3557	Sequence 3557, Ap
c 13	50	10.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 14	50	10.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c 15	50	10.3	1830121	4	US-10-329-960-1	Sequence 1, Appli
c 16	48	9.9	1141	4	US-09-806-708B-22	Sequence 22, Appl
c 17	46	9.4	6124	3	US-08-211-419B-3	Sequence 3, Appli
c 18	44.6	9.2	1493	1	US-08-340-820-24	Sequence 24, Appl
c 19	44.6	9.2	1493	1	US-08-593-535-24	Sequence 24, Appl
c 20	44.6	9.2	5152	1	US-10-204-708-73	Sequence 73, Appl
c 21	44.4	9.1	731	1	US-08-451-405A-2	Sequence 2, Appli
c 22	43	8.8	1850	3	US-08-617-860B-32	Sequence 32, Appl
c 23	43	8.8	4098	2	US-08-605-106-4	Sequence 1, Appli
c 24	42.6	8.7	640681	4	US-09-790-988-1	Sequence 1, Appli
c 25	42.2	8.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
c 26	42.2	8.7	2434	4	US-09-489-847-67	Sequence 67, Appl
c 27	42.2	8.7	3165	4	US-09-601-198-102	Sequence 102, App

c 28	42	8.6	19124	2	US-08-487-826B-13	Sequence 13, Appl
c 29	41.6	8.5	1141	4	US-09-806-708B-22	Sequence 22, Appl
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31	41.6	8.5	4687	4	US-09-978-522-2	Sequence 2, Appli
32	41.2	8.5	1263	4	US-09-540-236-1316	Sequence 1316, Ap
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37	41	8.4	6669	4	US-10-204-708-5	Sequence 5, Appli
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c 42	40.8	8.4	5562	4	US-10-204-708-64	Sequence 64, Appl
c 43	40.8	8.4	640681	4	US-09-790-988-1	Sequence 1, Appli
c 44	40.6	8.3	342	4	US-09-513-99C-19102	Sequence 19102, A
c 45	40.6	8.3	881	4	US-09-270-767-11666	Sequence 11666, A

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RESULT 1
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; Patent No. 6552927
; GENERAL INFORMATION:
; APPLICANT: ARONHEIM, AMI
; TITLE OF INVENTION: METHOD FOR DETECTION PROTEIN-PROTEIN INTERACTIONS AND A KIT TH;
; FILE REFERENCE: 108387.01
; CURRENT APPLICATION NUMBER: US/09/765,298A
; CURRENT FILING DATE:  2001-01-22
; PRIOR APPLICATION NUMBER: IL 125456
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: IL 128017
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 8001
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-765-298A-29

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                GenCore version 5.1.6
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Title:           US-09-903-508A-3
Perfect score:   487
Sequence:        1 tgattacgaattcgagtcg........agttcatgatttctgtta 487

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                 Gapop 10.0 , Gapext 1.0

Searched:        3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters:        7390102

Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	DB Length	ID	Description
1	486	99.8	487	10	487	US-09-903-508A-3	Sequence 3, Appl
2	457	93.8	1493	10	1493	US-09-903-508A-1	Sequence 1, Appli
3	211	43.3	8001	9	8001	US-10-765-298A-29	Sequence 29, Appl
c 4	206	42.3	11198	17	11201	US-10-776-213-23	Sequence 23, Appl
c 5	206	42.3	11201	17	11204	US-10-776-213-25	Sequence 25, Appl
c 6	206	42.3	11204	17	11427	US-10-776-213-26	Sequence 26, Appl
c 7	206	42.3	11427	17	12008	US-10-776-213-24	Sequence 24, Appl
c 8	206	42.3	12008	17	12844	US-10-776-213-27	Sequence 27, Appl
c 9	206	42.3	12844	17	12850	US-10-776-213-19	Sequence 19, Appl
c 10	206	42.3	12850	17	12851	US-10-776-213-22	Sequence 22, Appl
c 11	206	42.3	12851	17	13073	US-10-776-213-21	Sequence 21, Appl
c 12	206	42.3	13073	17	13654	US-10-776-213-20	Sequence 20, Appl
c 13	206	42.3	13654	17		US-10-776-213-28	Sequence 28, Appl
14	189.8	39.0	8800	17		US-10-450-097-29	Sequence 29, Appl
15	189.8	39.0	10040	17		US-10-450-097-30	Sequence 30, Appl
c 16	188.4	38.7	11365	18		US-10-433-311A-17	Sequence 17, Appl
c 17	176.2	36.2	9952	18		US-10-475-443-10	Sequence 10, Appl
18	120	24.6	1494	15		US-10-475-311-16	Sequence 16, Appl
19	71	14.6	1467	15		US-10-032-585-6216	Sequence 6216, Ap
20	62	12.7	312	17		US-10-767-701-26953	Sequence 26953, A
21	53	10.9	1554	15		US-10-128-714-7070	Sequence 7070, Ap
22	53	10.9	1778	15		US-10-128-714-6070	Sequence 6070, Ap
23	53	10.9	3140	15		US-10-128-71-70	Sequence 70, Appl
24	53	10.9	3778	15		US-10-128-714-5070	Sequence 5070, Ap
c 25	51	10.5	3673778	15		US-10-312-841-2	Sequence 2, Appli
c 26	50.6	10.4	467	17		US-10-021-323-6541	Sequence 6541, Ap
c 27	50.6	10.4	3673778	15		US-10-312-841-1	Sequence 1, Appli
c 28	50.4	10.3	1373	18		US-10-849-901-3	Sequence 3, Appli
29	50.2	10.3	531	17		US-10-021-323-6375	Sequence 6375, App
c 30	50.2	10.3	38342	16		US-10-221-714A-471	Sequence 471, App
c 31	50	10.3	6236	15		US-10-311-445-1604	Sequence 1604, Ap
c 32	50	10.3	1830121	14		US-10-329-960-1	Sequence 1, Appli
c 33	50	10.3	1830121	16		US-10-329-670-1	Sequence 1, Appli
c 34	50	10.3	1830121	18		US-10-158-865-1	Sequence 1, Appli
c 35	49.8	10.2	462	18		US-10-425-115-171081	Sequence 171081,
c 36	49.4	10.1	627	13		US-10-027-632-39761	Sequence 39761, A
c 37	49.4	10.1	627	15		US-10-027-63-39761	Sequence 39761, A
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c 39	47.6	9.8	7047	15		US-10-240-453-260	Sequence 260, App
c 40	47.2	9.7	349	10		US-09-814-35-18039	Sequence 18039, A
41	47.2	9.7	586	13		US-10-027-632-1415	Sequence 1415, Ap
42	47.2	9.7	586	15		US-10-027-632-1415	Sequence 1415, Ap
c 43	47.2	9.7	6308	15		US-10-311-455-1444	Sequence 1444, Ap
44	47.2	9.7	8056	18		US-10-473-126-386	Sequence 386, App
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ALIGNMENTS

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; Sequence 3, Application US/09903508A
; Publication No. US2003008215A1
; GENERAL INFORMATION:
;  APPLICANT: Abbas, Charles
;  APPLICANT: Voronovsky, Andrii
;  APPLICANT: Kshanovska, Barbara
;  APPLICANT: Fayura, Liubov
;  APPLICANT: Sibirna, Kateryna
;  APPLICANT: Sibirny, Andrii
;  APPLICANT: Dmytruk, Kostiantyn
;  TITLE OF INVENTION: Transformation Systems for Flavinogenic Yeast
;  FILE REFERENCE: 1533_0830003
;  CURRENT APPLICATION NUMBER: US/09/903,508A
;  CURRENT FILING DATE: 2002-06-26
;  PRIOR APPLICATION NUMBER: US 60/218,244
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 60/288,491
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: US 60/290,667
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 3
;  LENGTH: 487
;  TYPE: DNA
;  ORGANISM: Candida famata
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (415)..(415)
;  OTHER INFORMATION: May be any nucleotide
US-09-903-508A-3

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          GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    December 7, 2004, 20:16:14 ; Search time 2417 Seconds
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Title:          US-09-903-508A-3
Perfect score:  487
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Scoring table:  IDENTITY.NUC
                Gapop 10.0 , Gapext 1.0

Searched:       3282875 seqs, 1821986908 residues

Total number of hits satisfying chosen parameters:  65645750

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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             7: gb_est6:*
             8: gb_gss1:*
             9: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	4	88.2	18.1	938	9	CNS06L3M	AL403688 T7 end of
	5	80.4	16.5	903	9	CNS06O23	AL407521 T3 end of
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	7	62.2	12.8	1027	9	CNS02T50	AL212733 Tetraodon
	8	62	12.7	312	2	AW282691	AW282691 LG1_303_A
	9	59.4	12.2	928	9	CNS00DKY	AL071865 Drosophil
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	15	57.2	11.7	1045	9	CNS03YE4	AL266197 Tetraodon
	16	56.8	11.7	867	9	CNS00CX5	AL060052 Drosophil
	17	55.4	11.4	970	9	CNS0182E	AL108800 Drosophil
	18	54.8	11.3	1167	9	CNS07360	AL427102 clone BA0
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c	21	54.4	11.2	987	9	CNS0I4PQ	AL104456 Drosophil
c	22	54.4	11.2	1225	9	CNS0161D	AL106171 Drosophil
c	23	53.6	11.0	935	9	CNS01G4	AL098926 Drosophil
c	24	52.8	10.8	1023	9	CNS06ROO	AL411358 T3 end of
	25	52.8	10.8	1101	9	CNS002BM	AL097468 Drosophil
c	26	52.8	10.8	1728	3	CR719759	CR719759 Tetraodon
c	27	52.6	10.8	524	9	CNS01U9O	AL167541 Tetraodon
	28	52.4	10.8	878	9	AG595634	AG595634 Mus muscu
	29	52.4	10.8	893	9	CNS013XE	AL103436 Drosophil
c	30	52.4	10.8	973	9	CNS0080F	AL052232 Drosophil
c	31	52.4	10.8	1101	9	CNS002FG	AL062437 Drosophil
c	32	52.2	10.7	1092	9	CNS020K7	AL175696 Tetraodon
c	33	52	10.7	581	9	CNS034DK	AL227297 Tetraodon
c	34	52	10.6	1011	9	CNS01510	AL104886 Drosophil
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	36	51.6	10.6	911	8	BH161117	BH161117 ENTRB05TF
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	42	51	10.5	1200	9	CNS016CO	AL106578 Drosophil
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ALIGNMENTS

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VERSION     AQ639565.1  GI:5116275
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  ORGANISM  Trypanosoma brucei
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            Trypanosoma.
REFERENCE   1  (bases 1 to 722)
  AUTHORS   El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
            Gerrard,C., Leech,V., de Jong,P., Ulu,E., Melville,S.,
            Donelson,J., Fraser,C. and Adams,M.
  TITLE     Determination of clone end sequences from Trypanosoma brucei TREU
            927/4 P1 library
  JOURNAL   Unpublished (1999)
COMMENT     Other GSSs: 927P1-13A5.TP
            Contact: Najib M. El-Sayed
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: nelsayed@tigr.org
            For clone/filter availability, please contact Sara Melville
            (sm16@mole.bio.cam.ac.uk). P1 end sequences search page:
            http://www.tigr.org/tdb/mdb/tbdb/.
            Seq primer: T7
            Class: P1 ends.
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                     /mol_type="genomic DNA"
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                     /db_xref="taxon:5691"
                     /clone="927P1-13A5"
                     /clone_lib="927P1"
                     /note="Vector: pAD10SacBII; Site 1: Bam H1; Constructed by
                     Sara Melville, University of Cambridge, UK and Nancy
                     Shepherd, Dupont Merck, Wilmington, DE. Genomic DNA was
                     isolated from Trypanosoma brucei (stock TREU927/4) and
                     partially digested with Sau 3AI. DNA fragments were cloned
                     into the Bam H1 site of pAD10SacBII vector (Genbank
                     accession U09128). The average insert size is 65 Kb.
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